

FIGURE 1

47 kDa protein sequence, noon Apr 15, 2003

MW 45936.94 average, 421 aa, 93 % sequence coverage (confirmed residues indicated in red). @S indicates acetylation of the N-terminal serine residue (yielding a mass change +42.011 Da)

1 @SDNGPQSNQR SAPRITFGGP TDSTDNNQNG GRNGARPKQR RPQGLPNNNTA SWFTALTQHG
61 KEELRFPRGQ GVPINTNSGP DDQIGYYRRA TRRVRGGDGK **M**KELSPRWYF YYLGTGPEAS
121 LPYGANKEGI VWVATEGALN TPKDHIGTRN PNNNAATVLQ LPQGTTLPKG FYAEGSRGGS
181 QASSRSSRS RGNSRNSTPG SSRGNSPAR**M** ASGGGETALA LLLDLRLNQL ESKVSGKGQQ
241 QQGQTVTKS AAEASKKPRQ KRTATKQYNV TQAFRRRGPE QTQGNFGDQD LIRQGTDYKH
301 WPQIAQFAPS ASAFFG**MS**RI GMEVTPSGTW LTYHGAIKLD DKDPQFKDNV ILLNKHIDAY
361 KTFPPTEPKK DKKKKKTDEAQ PLPQRQKKQP TVTLLPAADM DDFSRQLQNS **MSG**ASADSTQ
421 A

FIGURE 2

SARS protein 139 kDa

FIFLLFL TLTSGLDLDR CTTFDDVQAP NYTQHTSSMR GVYYPDEIFR SDTLYLTQDL
 FLPFYSNVTG FHTINHTEGN PVIPFKDGIY FAATEKSNVV RGWVEFGSTMN NKSQSIIIN
 NSTNVVIRAC NFELCDNPFF AVSKPMGTQT HTMIFDNAFN CTFEYISDAF SLDVSEKSGN
 FKHLREFVFK NKDGFLYVYK GYQPIDVVRD LPSGFNTLKP IFKLPLGINI TNFRAILTAF
 SPAQDIWGTS AAAYFVGYLK PTTFMLKYDE NGTITDAVDC SQNPLAELKC SVKSFEIDKG
 IYQTSNFRVV PSGDVVRFPN ITNLCPFGEV FNATKFPSVY AWERKKISNC VADYSVLVNS
 TFFSTFKCYG VSATKLNDLC FSNVYADSFV VKGDDVRQIA PGQTGVIADY NYKLPDDFMG
 CVLAWNTRNI DATSTGNVNY KYRYLRHGKL RPFERDISNV PFSPDGKPCT PPALNCYWPL
 NDYGFYTTTG IGYQPYRVVV LSFELLNAPA TVCGPKLSTD LIKNQCVNFN FNGLTGTGVL
 TPSSKRFQPF QQFGRDVSDF TDSVRDPKTS EILDISPCAF GGVSVITPGT NASSEVAVLY
 QDVNCTDVST AIHADQLTPA WRIYSTGNNV FQTQAGCLIG AEHVDTSEYEC DIPIGAGICA
 SYHTVSLRLS TSQKSIVAYT MSLGADSSIA YSNNTIAIPT NFSISITTEV MPVSMAKTSV
 DCNMYICGDS TECANLLLQY GSFCTQLNRA LSGIAAEQDR NTREVEAQVK QMYKTPTLKY
 FGGFNFSQIL PDPLKPTKRS FIEDLLFNKV TLADAGFMKQ YGECLGDINA RDLICAQKFN
 GLTVLPPLLT DDMIAAYTAA LVSGTATAGW TFGAGAALQI PFAMQMAYRF NGIGVTQNVL
 YENQKQIANQ FNKAISQIQE SLTTTSTALG KLQDVVNQNA QALNTLVKQL SSNFGAISSV
 LNDILSRDLK VEAQVQIDRL ITGRLQSLQT YVTQQLIRAA EIRASANLAA TKMSECVLGQ
 SKRVDFCGKG YHLMSEFPQAA PHGVVFLHVT YVPSQERNFT TAPAICHEGK AYFPREGVFE
 FNGTSWFITQ RNFFSPQIIT TDNTFVSGNC DVVIGIINNT VYDPLQPELD SFKEELDKYF
 KNHTSPDVL GDISGINASV VNIQKEIDRL NEVAKNLNES LIDLQELGKY EQYIKWPWYV
 WLGFIAGLIA IVMVTILLCC MTSCCCLKG ACSCGSCCKF DEDDSEPVLK GVKLHYT

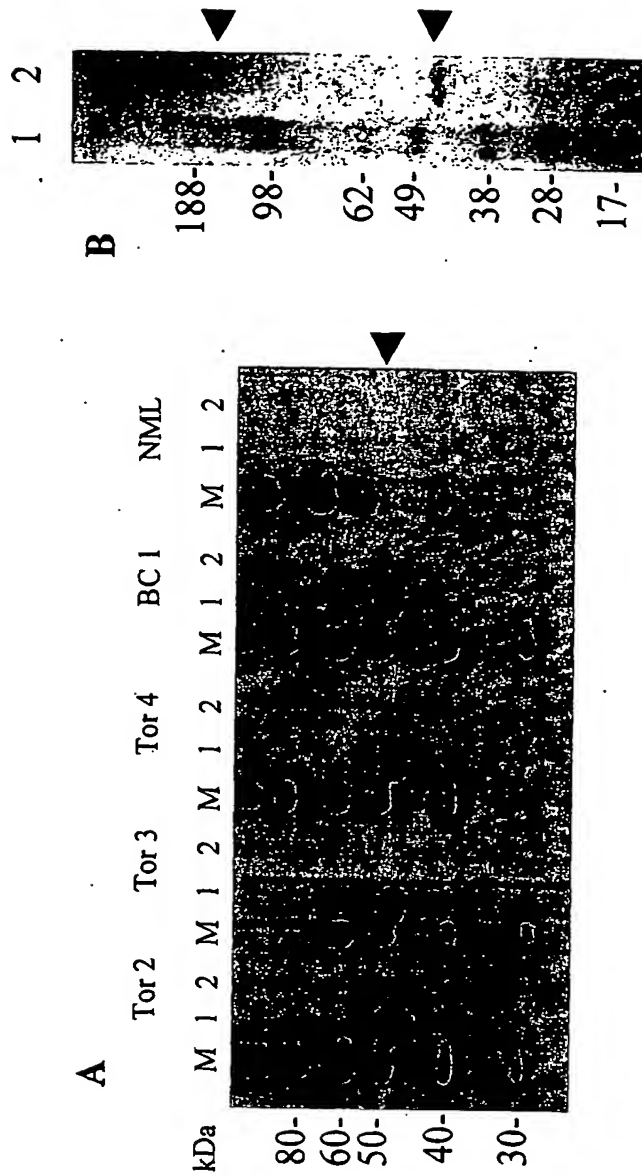


FIGURE 3

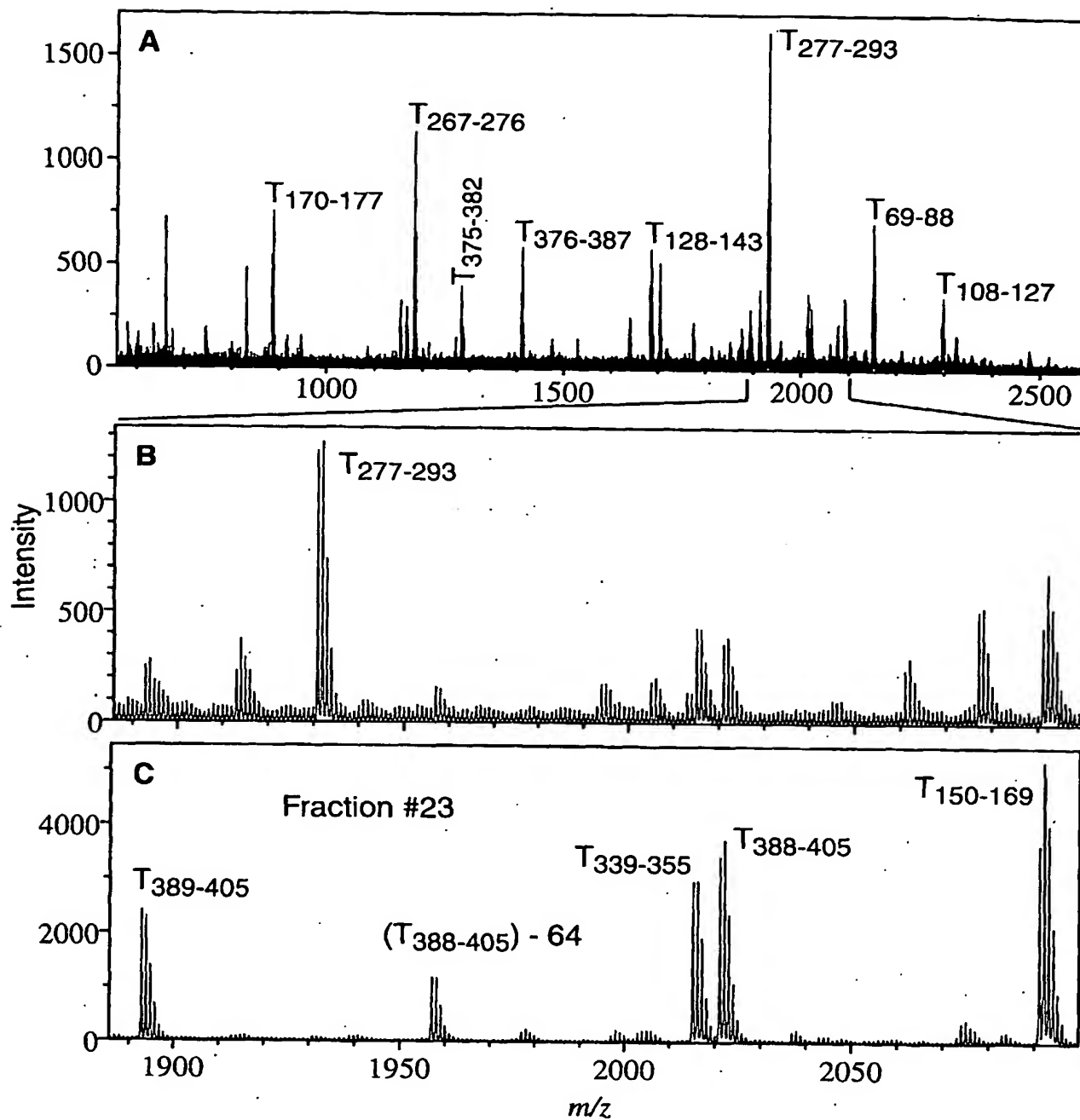


FIGURE 4

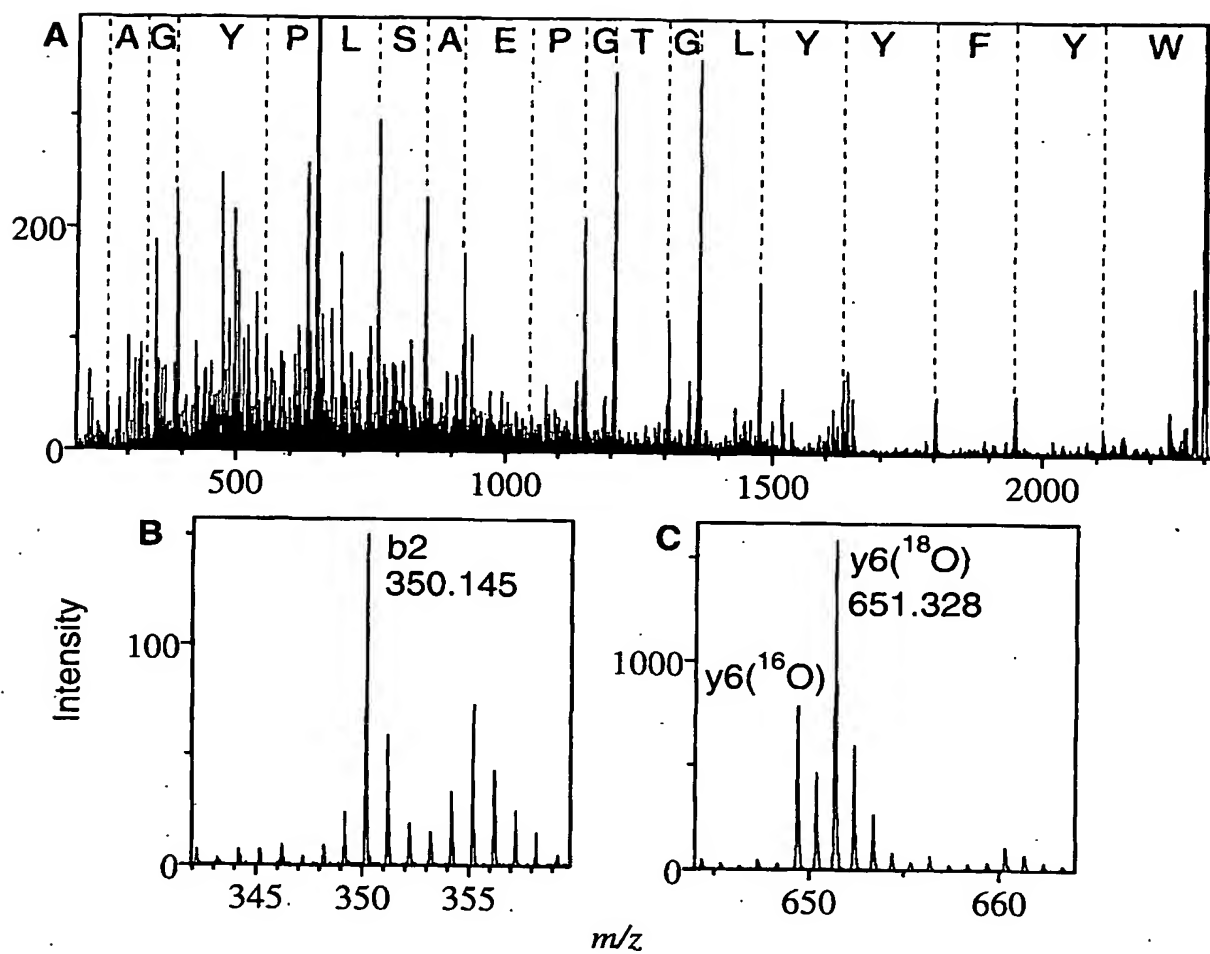


FIGURE 5

Coronavirus Nucleocapsid Protein Homology

| | | | |
|-----|---------------------|-----|---------|
| ... | WYFYLLGTGPEASLPYGAN | ... | SARS |
| ... | WYFYLLGTGPHAKDQYGTD | ... | Human |
| ... | WYFYLLGTGPHAKDQYGTD | ... | Bovine |
| ... | WYFYLLGTGPHAKDQYGTD | ... | Turkey |
| ... | WYFYLLGTGPHAKHQYGTD | ... | Porcine |
| ... | WYFYLLGTGPHAKAQYGTN | ... | Equine |
| ... | WYFYLLGTGPHAGASYGDD | ... | Murine |
| ... | WYFYLLGTGPHAGASFGDS | ... | Rat |

FIGURE 6

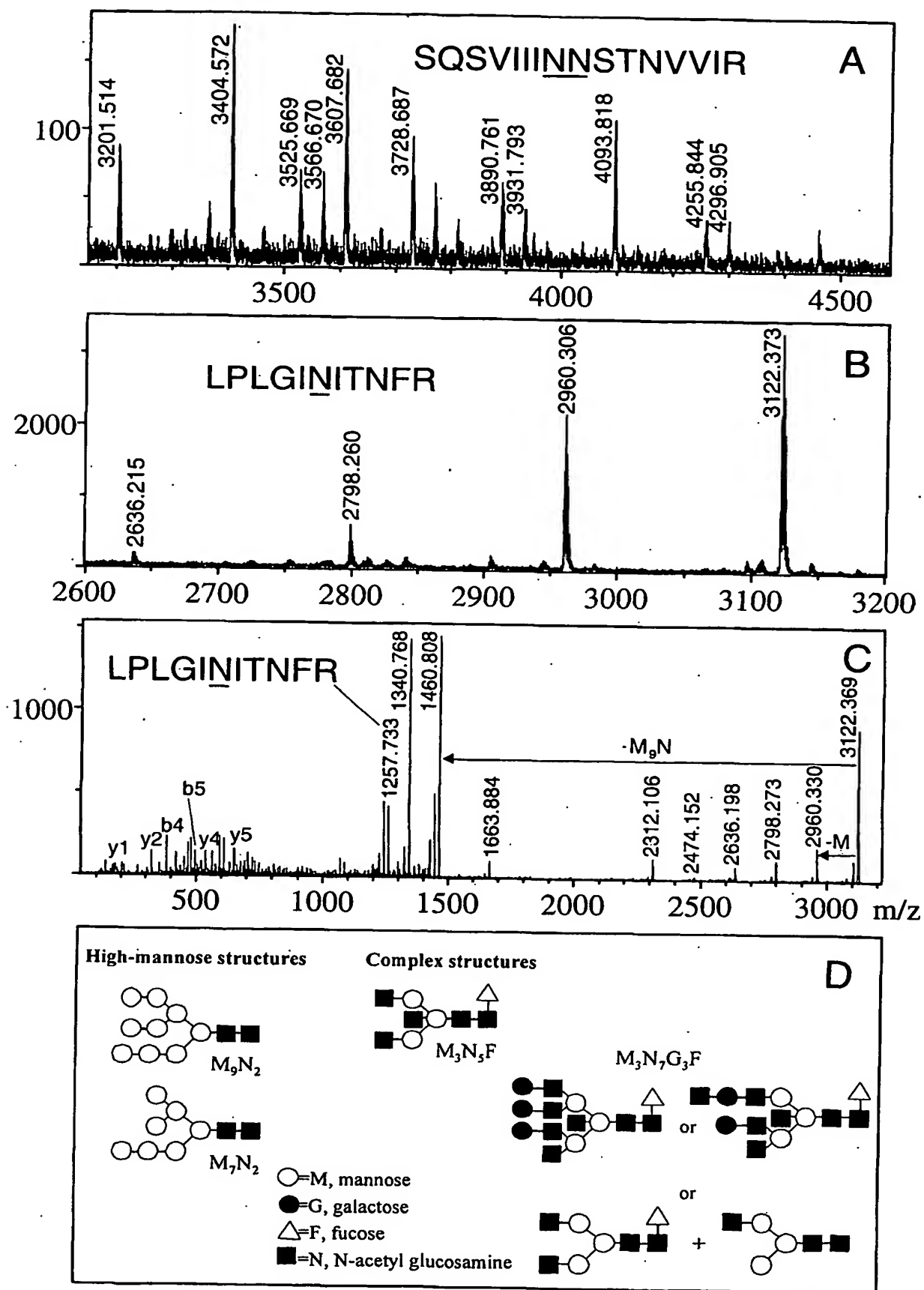


FIGURE 7

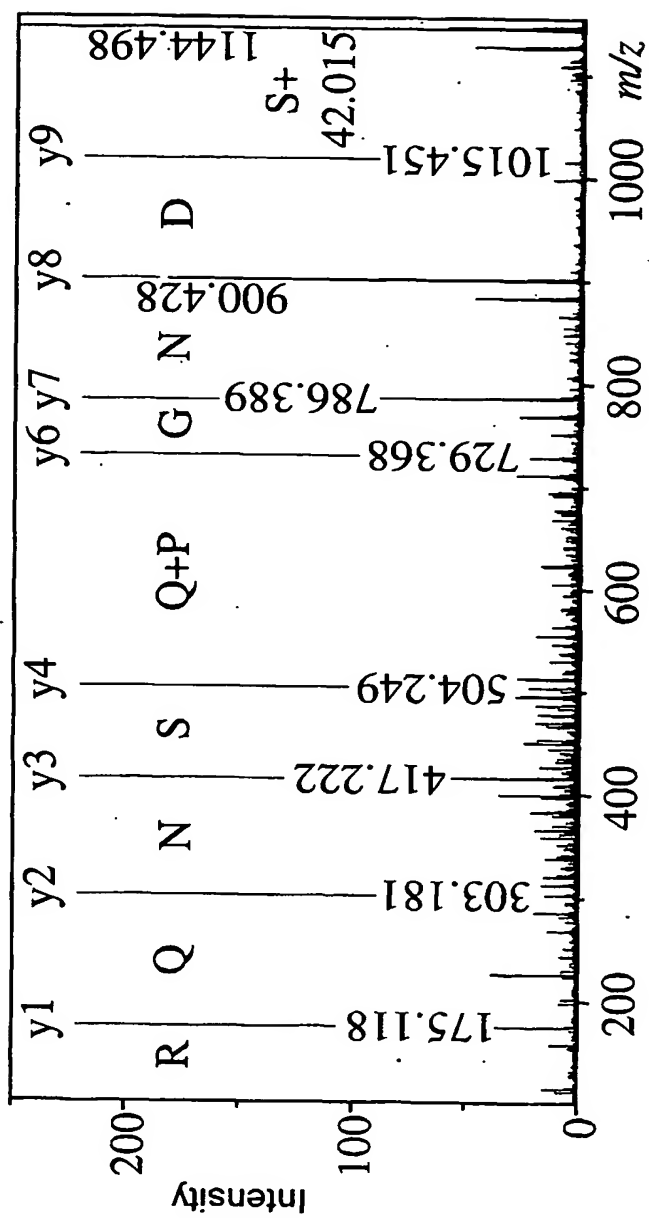


FIGURE 8

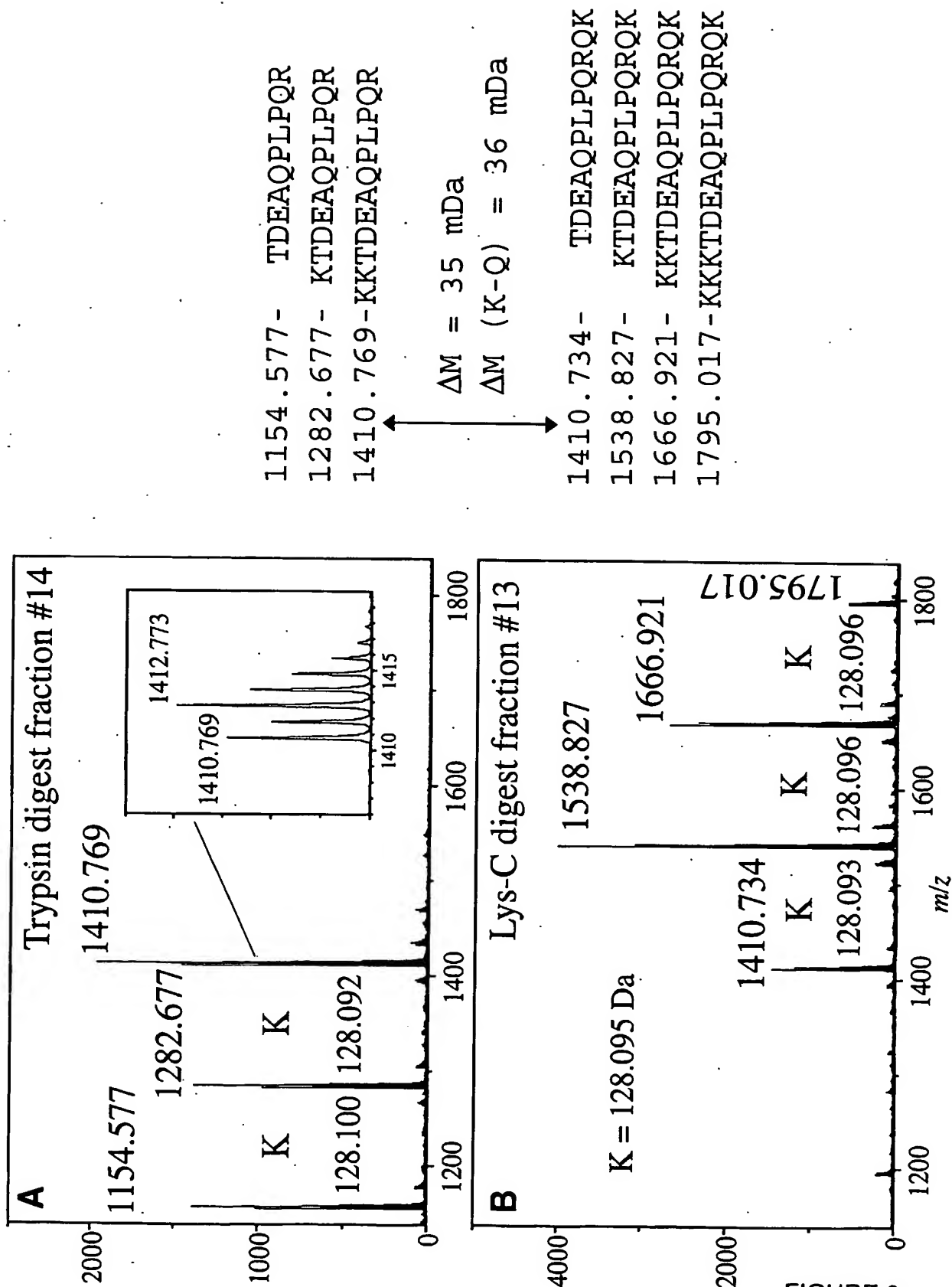


FIGURE 9

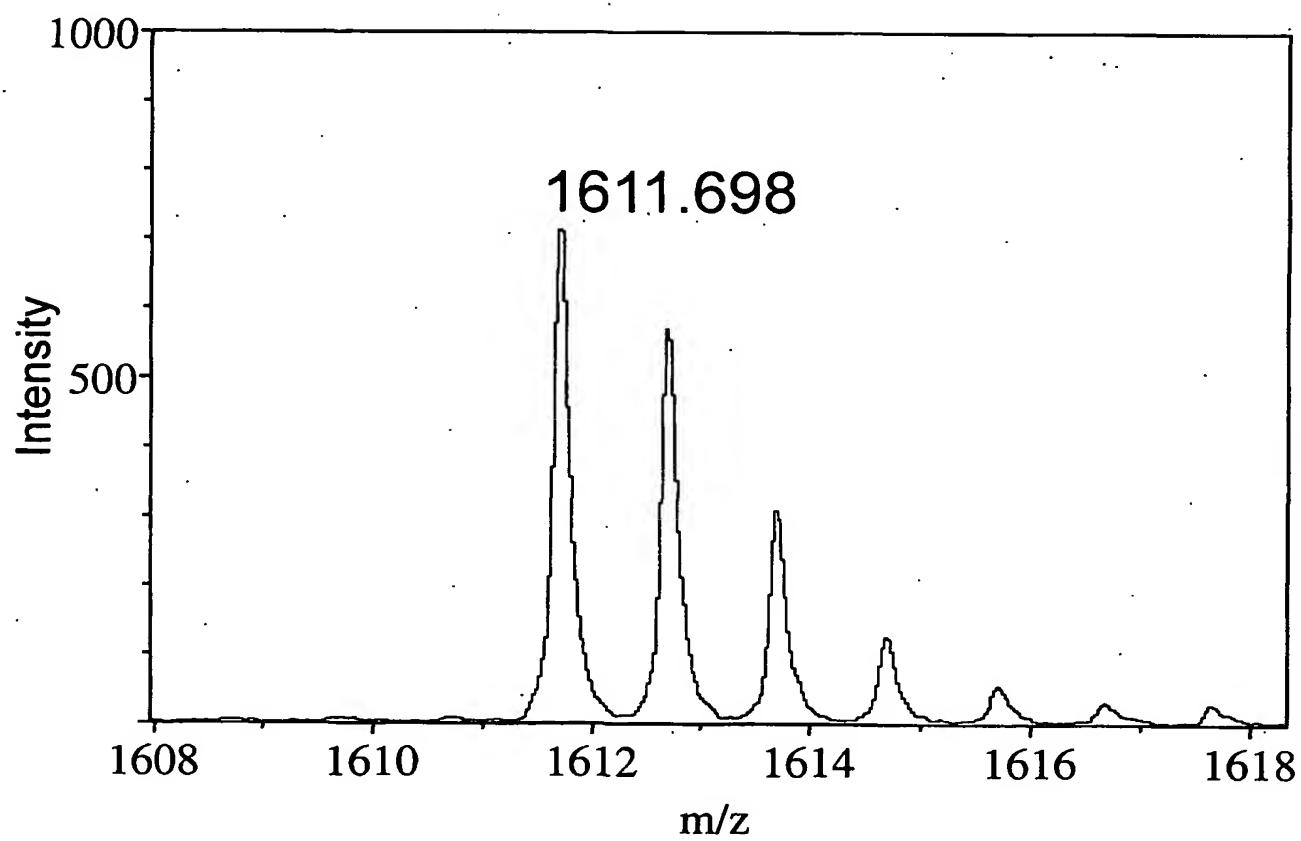


FIGURE 10

A

1 SDNGPQSNQR SAPRITFGGP TDSTDNNQNG GRNGARPKQR RPQGLPNNTA SWFTALTQHG
61 KEELRFPGRQ GVPINTNSGP DDQIGYYRRA TRVRGGDGK MKELSPRWYF YYLGTGPEAS
121 LPYGANKEGI VWVATEGALN TPKDHIGTRN PNNNAATVLQ LPQGTTLPGK FYAEGSRGGS
181 QASSRSSSRG EGNRRNSTPG SRRNSPARM ASGGGETALA LLLDLRLNQL ESKVSGKGQQ
241 QQGQTVTKKS AAEASKKPRQ KRTATKQYNV TQAFGRGPE QTQGNFGDQD LIRQGTDYKH
301 WPQIAQFAPS ASAFFGMSRI GMEVTPSGTW LTYHGAIKLD DKDPQFKDNV ILLNKHIDAY
361 KTFPPTEPKK DKKKKTDEAQ PLPQRQKKQP TVTLLPAADM DDFSRLQNS MSGASADSTQ
421 A

B

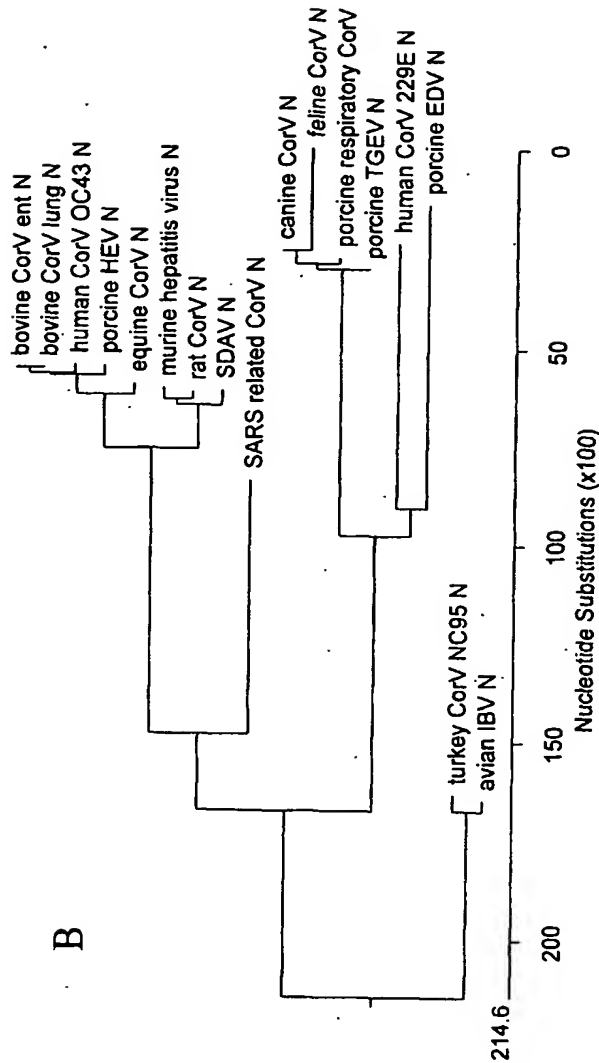


FIGURE 11

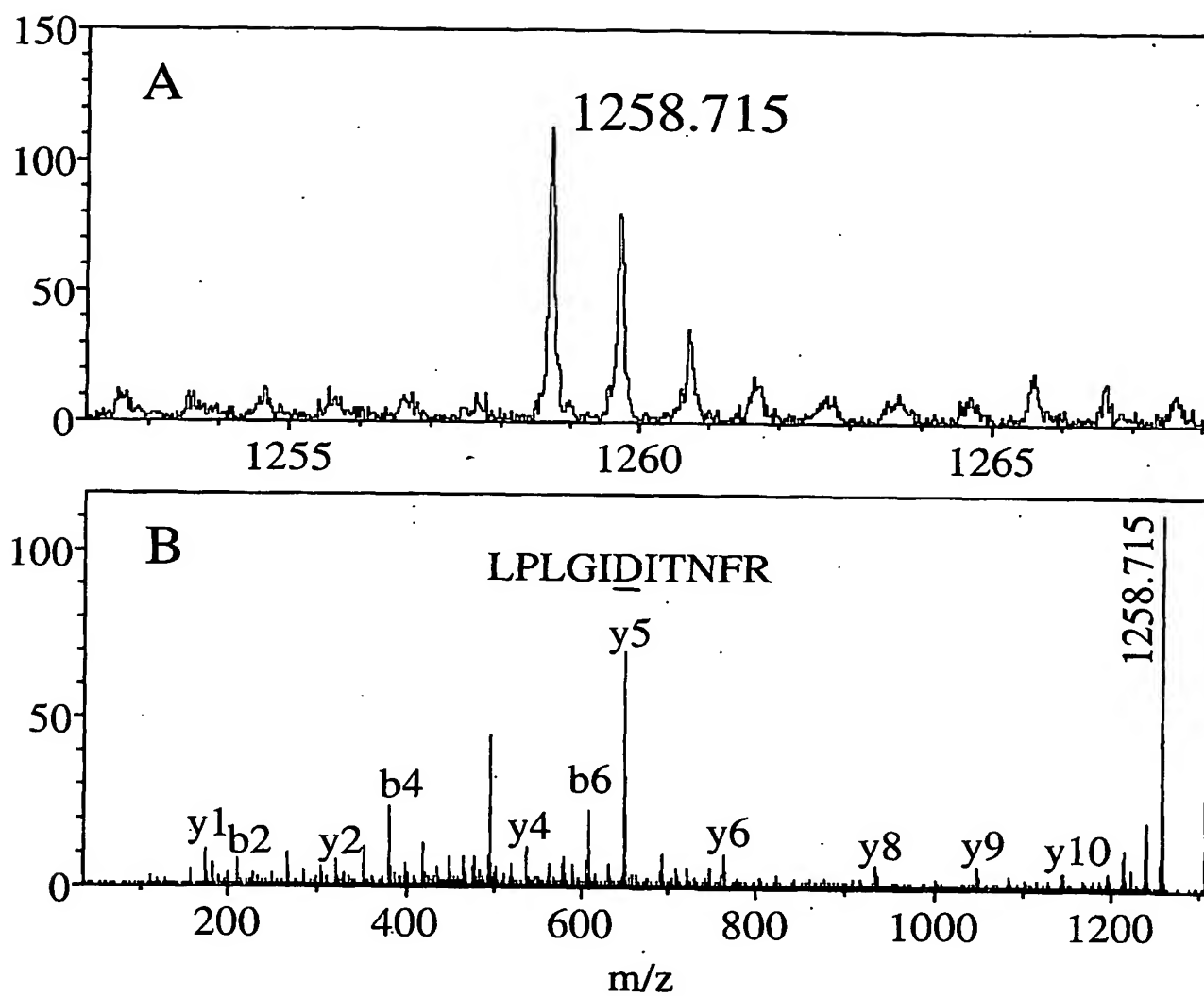


FIGURE 12